



SEQUENCE LISTING

<110> Sundelin, Johan
Scarborough, Robert M.

<120> Recombinant C140 Receptor, Its Agonists and Antagonists, and
Nucleic Acids Encoding the Receptor

<130> 44481-5006-09-US

<140> US 10/643,627

<141> 2003-08-19

<150> US 10/127,691

<151> 2002-04-23

<150> US 08/097,938

<151> 1993-07-26

<150> US 08/390,301

<151> 1995-01-25

<150> US 08/474,414

<151> 1995-06-07

<160> 64

<170> PatentIn Ver. 2.1

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<212> DNA

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<221> CDS

<222> (232)..(1416)

<223> C140 receptor, genomic DNA and deduced protein
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acacaagaat tagacttcaa ccgtcaccaa ctgccctgtg taggacggtc ggtcactgaa 180

agagaatatt gtctgcaata ctctaatac atctgtctgt gttcatctga a atg ttc 237
Met Phe

1

cat tta aaa cac agc agc ctt act gtt gga cca ttt atc tca gta atg 285
His Leu Lys His Ser Ser Leu Thr Val Gly Pro Phe Ile Ser Val Met

5

10

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Ile Leu Leu Arg Phe Leu Cys Thr Gly Arg Asn Asn Ser Lys Gly Arg

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agt ctt att ggc aga tta gaa acc cag cct cca atc act ggg aaa ggg			381
Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr Gly Lys Gly			
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gtt ccg gta gaa cca ggc ttt tcc atc gat gag ttc tct gcg tcc atc			429
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Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Val Val Tyr Ile Ile			
	70	75	80
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ctt ttc cga acg aag aag aaa cac ccc gcc gtg att tac atg gcc aac			573
Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile Tyr Met Ala Asn			
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ctg gcc ttg gcc gac ctc ctc tct gtc atc tgg ttc ccc ctg aag atc			621
Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe Pro Leu Lys Ile			
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Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala Leu Cys			
	135	140	145
aag gtg ctc att ggc ttt ttc tat ggt aac atg tat tgc tcc atc ctc			717
Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr Cys Ser Ile Leu			
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Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val Ile Val Asn Pro			
	165	170	175
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Met Gly His Pro Arg Lys Lys Ala Asn Ile Ala Val Gly Val Ser Leu			
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gca atc tgg ctc ctg att ttt ctg gtc acc atc cct ttg tat gtc atg			861
Ala Ile Trp Leu Leu Ile Phe Leu Val Thr Ile Pro Leu Tyr Val Met			
	195	200	205
aag cag acc atc tac att cca gca ttg aac atc acc acc tgt cac gat			909
Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys His Asp			
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Val Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr Phe Leu			
	230	235	240
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Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Leu Leu Thr Ala Ser			
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gcc tac gtg ctc atg atc aag acg ctc cgc tct tct gct atg gat gaa 1053
 Ala Tyr Val Leu Met Ile Lys Thr Leu Arg Ser Ser Ala Met Asp Glu
 260 265 270

cac tca gag aac aaa agg cag agg gct atc cga ctc atc atc acc gtg 1101
 His Ser Glu Lys Lys Arg Gln Arg Ala Ile Arg Leu Ile Ile Thr Val
 275 280 285 290

ctg gcc atg tac ttc atc tgc ttt gct cct agc aac ctt ctg ctc gta 1149
 Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro Ser Asn Leu Leu Leu Val
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gtg cat tat ttc cta atc aaa acc cag agg cag agc cac gtc tac gcc 1197
 Val His Tyr Phe Leu Ile Lys Thr Gln Arg Gln Ser His Val Tyr Ala
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ctc tac ctt gtc gcc ctc tgc ctg tcg acc ctc aac agc tgc ata gac 1245
 Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys Ile Asp
 325 330 335

ccc ttt gtc tat tac ttt gtc tca aaa gat ttc agg gat cac gcc aga 1293
 Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp Phe Arg Asp His Ala Arg
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Lys Gly Val Pro Val Glu Pro Gly Phe Ser Ile Asp Glu Phe Ser Ala
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Ser Ile Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Val Val Tyr
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 Ile Ile Val Phe Val Ile Gly Leu Pro Ser Asn Gly Met Ala Leu Trp
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 Ile Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile Tyr Met
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 Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe Pro Leu
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 Lys Ile Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala
 130 135 140
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 145 150 155 160
 Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val Ile Val
 165 170 175
 Asn Pro Met Gly His Pro Arg Lys Lys Ala Asn Ile Ala Val Gly Val
 180 185 190
 Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr Ile Pro Leu Tyr
 195 200 205
 Val Met Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys
 210 215 220
 His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr
 225 230 235 240
 Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Leu Leu Thr
 245 250 255
 Ala Ser Ala Tyr Val Leu Met Ile Lys Thr Leu Arg Ser Ser Ala Met
 260 265 270
 Asp Glu His Ser Glu Lys Lys Arg Gln Arg Ala Ile Arg Leu Ile Ile
 275 280 285
 Thr Val Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro Ser Asn Leu Leu
 290 295 300
 Leu Val Val His Tyr Phe Leu Ile Lys Thr Gln Arg Gln Ser His Val
 305 310 315 320
 Tyr Ala Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys
 325 330 335
 Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp Phe Arg Asp His
 340 345 350
 Ala Arg Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Asn Arg Met
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Ser Ser Ser Ser Thr Ser Val Lys Thr Ser Tyr
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<213> Homo sapiens

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<222> (56)..(1249)

<223> C140 receptor, genomic DNA and deduced protein
 sequences

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 Ser Val Met Thr Leu Val Phe Leu Ser Cys Thr Gly Thr Asn Arg Ser
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tct aaa gga aga agc ctt att ggt aag gtt gat ggc aca tcc cac gtc 202
 Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val
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act gga aaa gga gtt aca gtt gaa aca gtc ttt tct gtg gat gag ttt 250
 Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe
 50 55 60 65

tct gca tct gtc ctc act gga aaa ctg acc act gtc ttc ctt cca att 298
 Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Ile
 70 75 80

gtc tac aca att gtg ttt gtg gtg ggt ttg cca agt aac ggc atg gcc 346
 Val Tyr Thr Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met Ala
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ctg tgg gtc ttt ctt ttc cga act aag aag aag cac cct gct gtg att 394
 Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile
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 Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe
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Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly	
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Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr	
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Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val	
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Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile	
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Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile Pro	
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Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr	
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acc tgt cat gat gtt ttg cct gag cag ctc ttg gtg gga gac atg ttc	778
Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met Phe	
230 235 240	
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Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe	
245 250 255	
ctc aca gcc tct gcc tat gtg ctg atg atc aga atg ctg cga tct tct	874
Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser	
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Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu	
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Ile Val Thr Val Leu Ala Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn	
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Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg	
340 345 350	
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Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys
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 Gln Met Gln Val Ser Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser
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 Val Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu
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 Phe Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro
 65 70 75 80
 Ile Val Tyr Thr Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met
 85 90 95
 Ala Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val
 100 105 110
 Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp
 115 120 125
 Phe Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr
 130 135 140
 Gly Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met
 145 150 155 160
 Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp
 165 170 175
 Val Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala
 180 185 190
 Ile Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile
 195 200 205

Pro Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile
 210 215 220
 Thr Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met
 225 230 235 240
 Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala
 245 250 255
 Phe Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser
 260 265 270
 Ser Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys
 275 280 285
 Leu Ile Val Thr Val Leu Ala Met Tyr Leu Ile Cys Phe Thr Pro Ser
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 Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln
 305 310 315 320
 Ser His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu
 325 330 335
 Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe
 340 345 350
 Arg Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val
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<213> Mus musculus

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Lys Gly Val Pro Val Glu Pro Gly Phe Ser Ile Asp Glu Phe Ser Ala

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Ser	Ile	Leu	Thr	Gly	Lys	Leu	Thr	Thr	Val	Phe	Leu	Pro	Val	Val	Tyr
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Ile	Ile	Val	Phe	Val	Ile	Gly	Leu	Pro	Ser	Asn	Gly	Met	Ala	Leu	Trp
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Ile	Phe	Leu	Phe	Arg	Thr	Lys	Lys	Lys	His	Pro	Ala	Val	Ile	Tyr	Met
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Ala	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Ser	Val	Ile	Trp	Phe	Pro	Leu
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Lys	Ile	Ser	Tyr	His	Leu	His	Gly	Asn	Asn	Trp	Val	Tyr	Gly	Glu	Ala
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Leu	Cys	Lys	Val	Leu	Ile	Gly	Phe	Phe	Tyr	Gly	Asn	Met	Tyr	Cys	Ser
145					150					155					160
Ile	Leu	Phe	Met	Thr	Cys	Leu	Ser	Val	Gln	Arg	Tyr	Trp	Val	Ile	Val
				165					170					175	
Asn	Pro	Met	Gly	His	Pro	Arg	Lys	Lys	Ala	Asn	Ile	Ala	Val	Gly	Val
			180					185					190		
Ser	Leu	Ala	Ile	Trp	Leu	Leu	Ile	Phe	Leu	Val	Thr	Ile	Pro	Leu	Tyr
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Val	Met	Lys	Gln	Thr	Ile	Tyr	Ile	Pro	Ala	Leu	Asn	Ile	Thr	Thr	Cys
	210					215					220				
His	Asp	Val	Leu	Pro	Glu	Glu	Val	Leu	Val	Gly	Asp	Met	Phe	Asn	Tyr
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Phe	Leu	Ser	Leu	Ala	Ile	Gly	Val	Phe	Leu	Phe	Pro	Ala	Leu	Leu	Thr
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Ala	Ser	Ala	Tyr	Val	Leu	Met	Ile	Lys	Thr	Leu	Arg	Ser	Ser	Ala	Met
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Asp	Glu	His	Ser	Glu	Lys	Lys	Arg	Gln	Arg	Ala	Ile	Arg	Leu	Ile	Ile
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Thr	Val	Leu	Ala	Met	Tyr	Phe	Ile	Cys	Phe	Ala	Pro	Ser	Asn	Leu	Leu
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Leu	Val	Val	His	Tyr	Phe	Leu	Ile	Lys	Thr	Gln	Arg	Gln	Ser	His	Val
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Ala	Arg	Asn	Ala	Leu	Leu	Cys	Arg	Ser	Val	Arg	Thr	Val	Asn	Arg	Met

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 Val Thr Gly Lys Gly Val Ile Val Glu Ile Val Phe Ser Val Asp Glu
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 Phe Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro
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 Ile Val Tyr Ile Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met
 85 90 95

 Ala Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val
 100 105 110

 Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp
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 Phe Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr
 130 135 140

 Gly Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met
 145 150 155 160

 Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp
 165 170 175

 Val Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala
 180 185 190

 Ile Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile
 195 200 205

Pro Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile
 210 215 220
 Thr Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met
 225 230 235 240
 Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala
 245 250 255
 Phe Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser
 260 265 270
 Ser Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys
 275 280 285
 Leu Ile Val Thr Val Leu Ala Met Tyr Leu Ile Cys Phe Ile Pro Ser
 290 295 300
 Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln
 305 310 315 320
 Ser His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu
 325 330 335
 Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe
 340 345 350
 Arg Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val
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 Lys Gln Met Gln Val Ser Leu Ile Ser Lys Lys His Ser Arg Lys Ser
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 Ser Ser Tyr Ser Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr
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<211> 425

<212> PRT

<213> Mus musculus

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<223> Thrombin receptor

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 35 40 45

Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser
 50 55 60

Gly	Leu	Thr	Glu	Tyr	Arg	Leu	Val	Ser	Ile	Asn	Lys	Ser	Ser	Pro	Leu	65	70	75	80
Gln	Lys	Gln	Leu	Pro	Ala	Phe	Ile	Ser	Glu	Asp	Ala	Ser	Gly	Tyr	Leu	85	90	95	
Thr	Ser	Ser	Trp	Leu	Thr	Leu	Phe	Val	Pro	Ser	Val	Tyr	Thr	Gly	Val	100	105	110	
Phe	Val	Val	Ser	Leu	Pro	Leu	Asn	Ile	Met	Ala	Ile	Val	Val	Phe	Ile	115	120	125	
Leu	Lys	Met	Lys	Val	Lys	Lys	Pro	Ala	Val	Val	Tyr	Met	Leu	His	Leu	130	135	140	
Ala	Thr	Ala	Asp	Val	Leu	Phe	Val	Ser	Val	Leu	Pro	Phe	Lys	Ile	Ser	145	150	155	160
Tyr	Tyr	Phe	Ser	Gly	Ser	Asp	Trp	Gln	Phe	Gly	Ser	Glu	Leu	Cys	Arg	165	170	175	
Phe	Val	Thr	Ala	Ala	Phe	Tyr	Cys	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu	180	185	190	
Met	Thr	Val	Ile	Ser	Ile	Asp	Arg	Phe	Leu	Ala	Val	Val	Tyr	Pro	Met	195	200	205	
Gln	Ser	Leu	Ser	Trp	Arg	Thr	Leu	Gly	Arg	Ala	Ser	Phe	Thr	Cys	Leu	210	215	220	
Ala	Ile	Trp	Ala	Leu	Ala	Ile	Ala	Gly	Val	Val	Pro	Leu	Val	Leu	Lys	225	230	235	240
Glu	Gln	Thr	Ile	Gln	Val	Pro	Gly	Leu	Asn	Ile	Thr	Thr	Cys	His	Asp	245	250	255	
Val	Leu	Asn	Glu	Thr	Leu	Leu	Glu	Gly	Tyr	Tyr	Ala	Tyr	Tyr	Phe	Ser	260	265	270	
Ala	Phe	Ser	Ala	Val	Phe	Phe	Phe	Val	Pro	Leu	Ile	Ile	Ser	Thr	Val	275	280	285	
Cys	Tyr	Val	Ser	Ile	Ile	Arg	Cys	Leu	Ser	Ser	Ser	Ala	Val	Ala	Asn	290	295	300	
Arg	Ser	Lys	Lys	Ser	Arg	Ala	Leu	Phe	Leu	Ser	Ala	Ala	Val	Phe	Cys	305	310	315	320
Ile	Phe	Ile	Ile	Cys	Phe	Gly	Pro	Thr	Asn	Val	Leu	Leu	Ile	Ala	His	325	330	335	
Tyr	Ser	Phe	Leu	Ser	His	Thr	Ser	Thr	Thr	Glu	Ala	Ala	Tyr	Phe	Ala	340	345	350	
Tyr	Leu	Leu	Cys	Val	Cys	Val	Ser	Ser	Ile	Ser	Ser	Cys	Ile	Asp	Pro	355	360	365	

Leu Ile Tyr Tyr Tyr Ala Ser Ser Glu Cys Gln Arg Tyr Val Tyr Ser
370 375 380

Ile Leu Cys Cys Lys Glu Ser Ser Asp Pro Ser Ser Tyr Asn Ser Ser
385 390 395 400

Gly Gln Leu Met Ala Ser Lys Met Asp Thr Cys Ser Ser Asn Leu Asn
405 410 415

Asn Ser Ile Tyr Lys Lys Leu Leu Thr
420 425

<210> 8

<211> 7

<212> PRT

<213> Mus musculus

<220>

<223> C140 receptor activation peptide

<400> 8

Arg Asn Asn Ser Lys Gly Arg
1 5

<210> 9

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (1)

<223> Xaa at position 1 = 3-mercaptopropionic acid

<220>

<223> Description of Artificial Sequence: C140 receptor
antagonist

<400> 9

Xaa Leu Leu Gly Lys
1 5

<210> 10

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140
antagonist

<220>

<221> VARIANT

<222> (1)
 <223> Xaa at position 1 = 3-mercaptopropionic acid

 <400> 10
 Xaa Leu Ile Gly Arg
 1 5

 <210> 11
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

 <220>
 <221> VARIANT
 <222> (1)..(2)
 <223> Xaa at position 1 = 3-mercaptopropionic acid; Xaa
 at position 2 = cyclohexylalanine

 <400> 11
 Xaa Xaa Leu Lys Gly
 1 5

 <210> 12
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

 <220>
 <221> VARIANT
 <222> (1)..(2)
 <223> Xaa at position 1 = 3-mercaptopropionic acid; Xaa
 at position 2 = cyclohexylalanine

 <400> 12
 Xaa Xaa Ile Gly Arg
 1 5

 <210> 13
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

<220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 3-mercaptopropionic acid

 <400> 13
 Xaa Leu Leu Gly Lys Lys
 1 5

 <210> 14
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 3-mercaptopropionic acid

 <400> 14
 Xaa Leu Ile Gly Arg Lys
 1 5

 <210> 15
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 3-mercaptopropionic acid

 <400> 15
 Xaa Leu Ile Gly Arg Lys Glu Thr Gln Pro
 1 5 10

 <210> 16
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

<220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 3-mercaptopropionic acid

 <400> 16
 Xaa Leu Leu Gly Lys Lys Asp Gly Thr Ser
 1 5 10

 <210> 17
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = (n-pentyl) 2-N-Leu

 <400> 17
 Xaa Ile Gly Arg Lys
 1 5

 <210> 18
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = Me-N-(n-pentyl)

 <400> 18
 Xaa Leu Ile Gly Arg Lys
 1 5

 <210> 19
 <211> 12
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist/immunogen

<400> 19
Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr
1 5 10

<210> 20
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist/immunogen

<400> 20
Ile Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala Leu
1 5 10 15

Cys

<210> 21
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist/immunogen

<400> 21
Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys His Asp Val
1 5 10 15

Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr Phe Leu
20 25 30

<210> 22
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist/immunogen

<400> 22
His Tyr Phe Leu Ile Lys Thr Gln Arg Gln Ser His Val Tyr Ala
1 5 10 15

<210> 23
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 23
Ser Leu Ile Gly Arg Leu
1 5

<210> 24
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 24
Ser Leu Ile Gly Arg Ala
1 5

<210> 25
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 25
Ser Leu Ile Gly Ala Leu
1 5

<210> 26
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 26
Ser Leu Ile Ala Arg Leu
1 5

<210> 27
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor agonist

<400> 27
Ser Leu Ala Gly Arg Leu
1 5

<210> 28
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor agonist

<400> 28
Ser Ala Ile Gly Arg Leu
1 5

<210> 29
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor agonist

<400> 29
Ala Leu Ile Gly Arg Leu
1 5

<210> 30
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor agonist

<400> 30
Ser Phe Phe Leu Arg Trp
1 5

<210> 31
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 receptor agonist

<400> 31

Arg Asn Asn Ser Ser Lys Gly Arg
1 5

<210> 32

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 receptor agonist

<400> 32

Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr
1 5 10

<210> 33

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 receptor agonist

<400> 33

Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile
1 5 10

<210> 34

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 receptor agonist

<400> 34

Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro
1 5 10

<210> 35

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 receptor

agonist

<400> 35

Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro
1 5 10

<210> 36

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 36

Ser Leu Ile Gly Arg Leu Glu Thr Gln
1 5

<210> 37

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 agonist

<400> 37

Ser Leu Ile Gly Arg Leu Glu Thr
1 5

<210> 38

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 38

Ser Leu Ile Gly Arg Leu Glu
1 5

<210> 39

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 39
 Ser Leu Ile Gly Arg Leu
 1 5

<210> 40
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor agonist

<400> 40
 Ser Leu Ile Gly Arg
 1 5

<210> 41
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor agonist

<400> 41
 Ser Leu Leu Gly Lys Val Asp Gly Thr Ser His Val Thr
 1 5 10

<210> 42
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor agonist

<400> 42
 Ser Leu Leu Gly Lys Val Asp Gly Thr Ser His Val
 1 5 10

<210> 43
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor agonist

<400> 43

Ser Leu Leu Gly Lys Val Asp Gly Thr Ser His
1 5 10

<210> 44
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 44
Ser Leu Leu Gly Lys Val Asp Gly Thr Ser
1 5 10

<210> 45
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 45
Ser Leu Leu Gly Lys Val Asp Gly Thr
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 46
Ser Leu Leu Gly Lys Val Asp Gly
1 5

<210> 47
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 47
Ser Leu Leu Gly Lys Val Asp

1 5

<210> 48
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor agonist

<400> 48
 Ser Leu Leu Gly Lys Val
 1 5

<210> 49
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor agonist

<400> 49
 Ser Leu Leu Gly Lys
 1 5

<210> 50
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor agonist

<220>
 <221> VARIANT
 <222> (2)
 <223> Xaa at position 2 = cyclohexylalanine (Cha)

<400> 50
 Ser Xaa Ile Gly Arg
 1 5

<210> 51
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor

agonist

<220>
<221> VARIANT
<222> (2)
<223> Xaa at position 2 = cyclohexylalanine (Cha)

<400> 51
Ser Xaa Leu Gly Lys
1 5

<210> 52
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<220>
<221> VARIANT
<222> (1)
<223> Xaa at position 1 = 2,3-diamino propionic acid
(2,3-diaP)

<400> 52
Xaa Ile Gly Arg
1

<210> 53
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<220>
<221> VARIANT
<222> (1)
<223> Xaa at position 1 = 2,3-diamino propionic acid
(2,3-diaP)

<400> 53
Xaa Leu Leu Gly Lys
1 5

<210> 54
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 54
Ser Leu Leu Gly Lys Arg
1 5

<210> 55
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 55
Ser Leu Ile Gly Arg Arg
1 5

<210> 56
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<220>
<221> VARIANT
<222> (2)
<223> Xaa at position 2= cyclohexylalanine (Cha)

<400> 56
Ser Xaa Leu Gly Lys Lys
1 5

<210> 57
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 agonist
receptor

<220>
<221> VARIANT
<222> (2)
<223> Xaa at position 2 = cyclohexylalanine (Cha)

<400> 57

Ser Xaa Ile Gly Arg Lys
1 5

<210> 58
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<220>
<221> VARIANT
<222> (1)
<223> Xaa at position 1 = 2,3-diamino propionic acid
(2,3-diaP)

<400> 58
Xaa Leu Ile Gly Arg Lys
1 5

<210> 59
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<220>
<221> VARIANT
<222> (1)
<223> Xaa at position 1 = 2,3-diamino propionic acid
(2,3-diaP)

<400> 59
Xaa Leu Leu Gly Lys Lys
1 5

<210> 60
<211> 2732
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (73)..(1269)
<223> C140 receptor, cDNA and deduced protein sequences

<400> 60
ccctgtgctc agagtagggc tccgagtttc gaaccactgg tggcggattg cccgcccgcc 60

ccacgtccgg gg atg cga agt ctc agc ctg gcg tgg ctg ctg gga ggt atc 111
Met Arg Ser Leu Ser Leu Ala Trp Leu Leu Gly Gly Ile
1 5 10

acc ctt ctg gcg gcc tcg gtc tcc tgc agc cgg acc gag aac ctt gca 159
Thr Leu Leu Ala Ala Ser Val Ser Cys Ser Arg Thr Glu Asn Leu Ala
15 20 25

ccg gga cgc aac aac agt aaa gga aga agt ctt att ggc aga tta gaa 207
Pro Gly Arg Asn Asn Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Glu
30 35 40 45

acc cag cct cca atc act ggg aaa ggg gtt ccg gta gaa cca ggc ttt 255
Thr Gln Pro Pro Ile Thr Gly Lys Gly Val Pro Val Glu Pro Gly Phe
50 55 60

tcc atc gat gag ttc tct gcg tcc atc ctc acc ggg aag ctg acc acg 303
Ser Ile Asp Glu Phe Ser Ala Ser Ile Leu Thr Gly Lys Leu Thr Thr
65 70 75

gtc ttt ctt ccg gtc gtc tac att att gtg ttt gtg att ggt ttg ccc 351
Val Phe Leu Pro Val Val Tyr Ile Ile Val Phe Val Ile Gly Leu Pro
80 85 90

agt aat ggc atg gcc ctc tgg atc ttc ctt ttc cga acg aag aag aaa 399
Ser Asn Gly Met Ala Leu Trp Ile Phe Leu Phe Arg Thr Lys Lys Lys
95 100 105

cac ccc gcc gtg att tac atg gcc aac ctg gcc ttg gcc gac ctc ctc 447
His Pro Ala Val Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu
110 115 120 125

tct gtc atc tgg ttc ccc ctg aag atc tcc tac cac cta cat ggc aac 495
Ser Val Ile Trp Phe Pro Leu Lys Ile Ser Tyr His Leu His Gly Asn
130 135 140

aac tgg gtc tac ggg gag gcc ctg tgc aag gtg ctc att ggc ttt ttc 543
Asn Trp Val Tyr Gly Glu Ala Leu Cys Lys Val Leu Ile Gly Phe Phe
145 150 155

tat ggt aac atg tat tgc tcc atc ctc ttc atg acc tgc ctc agc gtg 591
Tyr Gly Asn Met Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val
160 165 170

cag agg tac tgg gtg atc gtg aac ccc atg gga cac ccc agg aag aag 639
Gln Arg Tyr Trp Val Ile Val Asn Pro Met Gly His Pro Arg Lys Lys
175 180 185

gca aac atc gcc gtt ggc gtc tcc ttg gca atc tgg ctc ctg att ttt 687
Ala Asn Ile Ala Val Gly Val Ser Leu Ala Ile Trp Leu Leu Ile Phe
190 195 200 205

ctg gtc acc atc cct ttg tat gtc atg aag cag acc atc tac att cca 735
Leu Val Thr Ile Pro Leu Tyr Val Met Lys Gln Thr Ile Tyr Ile Pro
210 215 220

gca ttg aac atc acc acc tgt cac gat gtg ctg cct gag gag gta ttg 783

Ala Leu Asn Ile Thr Thr Cys His Asp Val Leu Pro Glu Glu Val Leu
225 230 235

gtg ggg gac atg ttc aat tac ttc ctc tca ctg gcc att gga gtc ttc 831
Val Gly Asp Met Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe
240 245 250

ctg ttc ccg gcc ctc ctt act gca tct gcc tac gtg ctc atg atc aag 879
Leu Phe Pro Ala Leu Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Lys
255 260 265

acg ctc cgc tct tct gct atg gat gaa cac tca gag aag aaa agg cag 927
Thr Leu Arg Ser Ser Ala Met Asp Glu His Ser Glu Lys Lys Arg Gln
270 275 280 285

agg gct atc cga ctc atc atc acc gtg ctg gcc atg tac ttc atc tgc 975
Arg Ala Ile Arg Leu Ile Ile Thr Val Leu Ala Met Tyr Phe Ile Cys
290 295 300

ttt gct cct agc aac ctt ctg ctc gta gtg cat tat ttc cta atc aaa 1023
Phe Ala Pro Ser Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys
305 310 315

acc cag agg cag agc cac gtc tac gcc ctc tac ctt gtc gcc ctc tgc 1071
Thr Gln Arg Gln Ser His Val Tyr Ala Leu Tyr Leu Val Ala Leu Cys
320 325 330

ctg tcg acc ctc aac agc tgc ata gac ccc ttt gtc tat tac ttt gtc 1119
Leu Ser Thr Leu Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val
335 340 345

tca aaa gat ttc agg gat cac gcc aga aac gcg ctc ctc tgc cga agt 1167
Ser Lys Asp Phe Arg Asp His Ala Arg Asn Ala Leu Leu Cys Arg Ser
350 355 360 365

gtc cgc act gtg aat cgc atg caa atc tcg ctc agc tcc aac aag ttc 1215
Val Arg Thr Val Asn Arg Met Gln Ile Ser Leu Ser Ser Asn Lys Phe
370 375 380

tcc agg aag tcc ggc tcc tac tct tca agc tca acc agt gtt aaa acc 1263
Ser Arg Lys Ser Gly Ser Tyr Ser Ser Ser Ser Thr Ser Val Lys Thr
385 390 395

tcc tac tgagctgtac ctgaggatgt caagcctgct tgatgatgat gatgatgatg 1319
Ser Tyr

gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gcacccgtgt gtgagtgcgt 1379

ggtagggata caccaacatg gatggggctg tcatttctta tccaagctgt ctgtctctgc 1439

accaatcaca agcatgcagc tctccccagg attgacagaa gcctcctcct ttgcatgaga 1499

acagtcttcc actctgatga aaagcatcag tatcagaaac tgaaacgaac tgagaggagc 1559

ttgttttgtg aaagtgaaga gaagatggag ggtcagtgcac ttgcaaaaaa aaccaaccaa 1619

acaaaaacta cacctggcaa gaaggctaag actctctgaa atgcttcctt tttccatctg 1679

gagttcgtct cggccttggt caggacctga ggccctggta gagcttcagt ccagttgatt 1739
 gactttacag acttgagaga ggagtgaatg aggagtgaat gaggctcctg gcggcatcct 1799
 aaccggctaa cagtggcctt gctggacaat aggattcaga tggctggagt tacatttctca 1859
 caccatttca tcagaactat tggggatcct gatcaatgtg caggtcctt agcgtcagta 1919
 accctgggag ctcagacacg atgggggtga ggggtggggg gggggtgggg gtgaggctct 1979
 acaaacctta gtgatgactg cagacacaga accatggagc tgagcctgct tctgcttgcc 2039
 agggcaccac tgtaatgttg gcaaagaaaa accaacagca gtgttttgag cctctttttt 2099
 tggtcagttt atgatgaatt tgcctattgg tttattggga ttttcagttc ctttattact 2159
 ttgttgtaat tttgtgtgtt tattagtcaa gaaaaagaag atgaggctct taaaaatgta 2219
 aataaaattt ttggtttttt gggtttttta cttgggccaa ctacaaatac tgcttaggtt 2279
 tttttctaac ttaattgtta actacatcat gtgaacttaa gacattttca tgataaagca 2339
 ttactgtagt gtcagttttc cctcatcctc gatcatagtc cttcccgtga agcagggccc 2399
 ttcccctccc ccccctttgc cgtttccctc cccaccagat agtccccctg tctgctttaa 2459
 cctaccagtt agtattttat aaaaacagat cattggaata tttattatca gttttgttca 2519
 cttgttatca gttttgttca ctaatttgtc caataatgga attaacgtct tctcatctgt 2579
 ttgaggaaga tctgaaacaa ggggccattg caggagtaca tggctccagg cttactttat 2639
 atactgcctg tatttgtggc tttaaaaaaa tgaccttggt atatgaatgc tttataaata 2699
 aataatgcat gaactttaaa aaaaaaaaaa aaa 2732

<210> 61
 <211> 399
 <212> PRT
 <213> Mus musculus

<400> 61
 Met Arg Ser Leu Ser Leu Ala Trp Leu Leu Gly Gly Ile Thr Leu Leu
 1 5 10 15
 Ala Ala Ser Val Ser Cys Ser Arg Thr Glu Asn Leu Ala Pro Gly Arg
 20 25 30
 Asn Asn Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro
 35 40 45
 Pro Ile Thr Gly Lys Gly Val Pro Val Glu Pro Gly Phe Ser Ile Asp
 50 55 60
 Glu Phe Ser Ala Ser Ile Leu Thr Gly Lys Leu Thr Thr Val Phe Leu

370 375 380
 Ser Gly Ser Tyr Ser Ser Ser Ser Thr Ser Val Lys Thr Ser Tyr
 385 390 395

<210> 62
 <211> 1414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50)..(1240)
 <223> C140 receptor, cDNA and deduced protein sequences

<400> 62
 caaagaattg taatacgact cactataggg cgaattcgga tccaggagg atg cgg agc 58
 Met Arg Ser
 1

ccc agc gcg gcg tgg ctg ctg ggg gcc gcc atc ctg cta gca gcc tct 106
 Pro Ser Ala Ala Trp Leu Leu Gly Ala Ala Ile Leu Leu Ala Ala Ser
 5 10 15

ctc tcc tgc agt ggc acc atc caa gga acc aat aga tcc tct aaa gga 154
 Leu Ser Cys Ser Gly Thr Ile Gln Gly Thr Asn Arg Ser Ser Lys Gly
 20 25 30 35

aga agc ctt att ggt aag gtt gat ggc aca tcc cac gtc act gga aaa 202
 Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val Thr Gly Lys
 40 45 50

gga gtt aca gtt gaa aca gtc ttt tct gtg gat gag ttt tct gca tct 250
 Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe Ser Ala Ser
 55 60 65

gtc ctc gct gga aaa ctg acc act gtc ttc ctt cca att gtc tac aca 298
 Val Leu Ala Gly Lys Leu Thr Thr Val Phe Leu Pro Ile Val Tyr Thr
 70 75 80

att gtg ttt gcg gtg ggt ttg cca agt aac ggc atg gcc cta tgg gtc 346
 Ile Val Phe Ala Val Gly Leu Pro Ser Asn Gly Met Ala Leu Trp Val
 85 90 95

ttt ctt ttc cga act aag aag aag cac cct gct gtg att tac atg gcc 394
 Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile Tyr Met Ala
 100 105 110 115

aat ctg gcc ttg gct gac ctc ctc tct gtc atc tgg ttc ccc ttg aag 442
 Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe Pro Leu Lys
 120 125 130

att gcc tat cac ata cat ggc aac aac tgg att tat ggg gaa gct ctt 490
 Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly Glu Ala Leu
 135 140 145

tgt aat gtg ctt att ggc ttt ttc tat cgc aac atg tac tgt tcc att	538
Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr Cys Ser Ile	
150 155 160	
ctc ttc atg acc tgc ctc agt gtg cag agg tat tgg gtc atc gtg aac	586
Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val Ile Val Asn	
165 170 175	
ccc atg ggg cac tcc agg aag aag gca aac att gcc att ggc atc tcc	634
Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile Gly Ile Ser	
180 185 190 195	
ctg gca ata tgg ctg ctg act ctg ctg gtc acc atc cct ttg tat gtc	682
Leu Ala Ile Trp Leu Leu Thr Leu Leu Val Thr Ile Pro Leu Tyr Val	
200 205 210	
gtg aag cag acc atc ttc att cct gcc ctg aac atc acg acc tgt cat	730
Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr Thr Cys His	
215 220 225	
gat gtt ttg cct gag cag ctc ttg gtg gga gac atg ttc aat tac ttc	778
Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met Phe Asn Tyr Phe	
230 235 240	
ctc tct ctg gcc att ggg gtc ttt ctg ttc cca gcc ttc ctc aca gcc	826
Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe Leu Thr Ala	
245 250 255	
tct gcc tat gtg ctg atg atc aga atg ctg cga tct tct gcc atg gat	874
Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser Ala Met Asp	
260 265 270 275	
gaa aac tca gag aag aaa agg aag agg gcc atc aaa ctc att gtc act	922
Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu Ile Val Thr	
280 285 290	
gtc ctg ggc atg tac ctg atc tgc ttc act cct agt aac ctt ctg ctt	970
Val Leu Gly Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn Leu Leu Leu	
295 300 305	
gtg gtg cat tat ttt ctg att aag agc cag ggc cag agc cat gtc tat	1018
Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser His Val Tyr	
310 315 320	
gcc ctg tac att gta gcc ctc tgc ctc tct acc ctt aac agc tgc atc	1066
Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys Ile	
325 330 335	
gac ccc ttt gtc tat tac ttt gtt tca cat gat ttc agg gat cat gca	1114
Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg Asp His Ala	
340 345 350 355	
aag aac gct ctc ctt tgc cga agt gtc cgc act gta aag cag atg caa	1162
Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys Gln Met Gln	
360 365 370	

gta ccc ctc acc tca aag aaa cac tcc agg aaa tcc agc tct tac tct 1210
 Val Pro Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser Ser Tyr Ser
 375 380 385

tca agt tca acc act gtt aag acc tcc tat tgagttttcc aggtcctcag 1260
 Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr
 390 395

atgggaattg cacagtagga tgtggaacct gtttaatgtt atgaggacgt gtctgttatt 1320

tccggatcca gatcttatta aagcagaact tggtttattgc agcttataat gggtacaaat 1380

aaagcaatag catcacaaat ttcacaaata aagc 1414

<210> 63

<211> 397

<212> PRT

<213> Homo sapiens

<400> 63

Met Arg Ser Pro Ser Ala Ala Trp Leu Leu Gly Ala Ala Ile Leu Leu
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Ala Ala Ser Leu Ser Cys Ser Gly Thr Ile Gln Gly Thr Asn Arg Ser
 20 25 30

Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val
 35 40 45

Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe
 50 55 60

Ser Ala Ser Val Leu Ala Gly Lys Leu Thr Thr Val Phe Leu Pro Ile
 65 70 75 80

Val Tyr Thr Ile Val Phe Ala Val Gly Leu Pro Ser Asn Gly Met Ala
 85 90 95

Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile
 100 105 110

Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe
 115 120 125

Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly
 130 135 140

Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr
 145 150 155 160

Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val
 165 170 175

Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile
 180 185 190

Gly Ile Ser Leu Ala Ile Trp Leu Leu Thr Leu Leu Val Thr Ile Pro
 195 200 205
 Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr
 210 215 220
 Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met Phe
 225 230 235 240
 Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe
 245 250 255
 Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser
 260 265 270
 Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu
 275 280 285
 Ile Val Thr Val Leu Gly Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn
 290 295 300
 Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser
 305 310 315 320
 His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn
 325 330 335
 Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg
 340 345 350
 Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys
 355 360 365
 Gln Met Gln Val Pro Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser
 370 375 380
 Ser Tyr Ser Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr
 385 390 395

<210> 64
 <211> 425
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Gly Pro Arg Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys
 1 5 10 15
 Gly Pro Leu Leu Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys
 20 25 30
 Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro
 35 40 45
 Asn Asp Lys Tyr Glu Pro Glu Trp Glu Asp Glu Glu Lys Asn Glu Ser
 50 55 60

Gly	Leu	Thr	Glu	Tyr	Arg	Leu	Val	Ser	Ile	Asn	Lys	Ser	Ser	Pro	Leu	
65					70					75					80	
Gln	Lys	Gln	Leu	Pro	Ala	Phe	Ile	Ser	Glu	Asp	Ala	Ser	Gly	Tyr	Leu	
				85					90					95		
Thr	Ser	Ser	Trp	Leu	Thr	Leu	Phe	Val	Pro	Ser	Val	Tyr	Thr	Gly	Val	
			100					105					110			
Phe	Val	Val	Ser	Leu	Pro	Leu	Asn	Ile	Met	Ala	Ile	Val	Val	Phe	Ile	
		115					120					125				
Leu	Lys	Met	Lys	Val	Lys	Lys	Pro	Ala	Val	Val	Tyr	Met	Leu	His	Leu	
	130					135					140					
Ala	Thr	Ala	Asp	Val	Leu	Phe	Val	Ser	Val	Leu	Pro	Phe	Lys	Ile	Ser	
145					150					155					160	
Tyr	Tyr	Phe	Ser	Gly	Ser	Asp	Trp	Gln	Phe	Gly	Ser	Glu	Leu	Cys	Arg	
			165					170						175		
Phe	Val	Thr	Ala	Ala	Phe	Tyr	Cys	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu	
			180					185					190			
Met	Thr	Val	Ile	Ser	Ile	Asp	Arg	Phe	Leu	Ala	Val	Val	Tyr	Pro	Met	
		195					200					205				
Gln	Ser	Leu	Ser	Trp	Arg	Thr	Leu	Gly	Arg	Ala	Ser	Phe	Thr	Cys	Leu	
	210					215					220					
Ala	Ile	Trp	Ala	Leu	Ala	Ile	Ala	Gly	Val	Val	Pro	Leu	Val	Leu	Lys	
225					230					235					240	
Glu	Gln	Thr	Ile	Gln	Val	Pro	Gly	Leu	Asn	Ile	Thr	Thr	Cys	His	Asp	
			245						250					255		
Val	Leu	Asn	Glu	Thr	Leu	Leu	Glu	Gly	Tyr	Tyr	Ala	Tyr	Tyr	Phe	Ser	
			260					265					270			
Ala	Phe	Ser	Ala	Val	Phe	Phe	Phe	Val	Pro	Leu	Ile	Ile	Ser	Thr	Val	
		275					280					285				
Cys	Tyr	Val	Ser	Ile	Ile	Arg	Cys	Leu	Ser	Ser	Ser	Ala	Val	Ala	Asn	
	290					295					300					
Arg	Ser	Lys	Lys	Ser	Arg	Ala	Leu	Phe	Leu	Ser	Ala	Ala	Val	Phe	Cys	
305					310					315					320	
Ile	Phe	Ile	Ile	Cys	Phe	Gly	Pro	Thr	Asn	Val	Leu	Leu	Ile	Ala	His	
			325						330					335		
Tyr	Ser	Phe	Leu	Ser	His	Thr	Ser	Thr	Thr	Glu	Ala	Ala	Tyr	Phe	Ala	
			340					345					350			
Tyr	Leu	Leu	Cys	Val	Cys	Val	Ser	Ser	Ile	Ser	Ser	Cys	Ile	Asp	Pro	
		355					360					365				

Leu Ile Tyr Tyr Tyr Ala Ser Ser Glu Cys Gln Arg Tyr Val Tyr Ser
370 375 380

Ile Leu Cys Cys Lys Glu Ser Ser Asp Pro Ser Ser Tyr Asn Ser Ser
385 390 395 400

Gly Gln Leu Met Ala Ser Lys Met Asp Thr Cys Ser Ser Asn Leu Asn
405 410 415

Asn Ser Ile Tyr Lys Lys Leu Leu Thr
420 425